



**FACULTY OF ENGINEERING AND  
TECHNOLOGY**

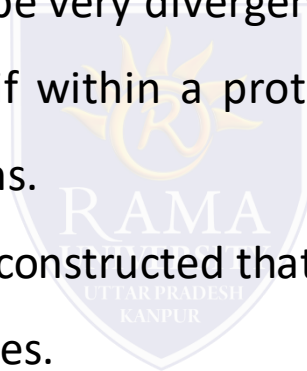
**Department of Biotechnology**

## Motif, Profiles, Patterns

- ✓ When aligning protein sequences it is often apparent that certain regions or specific amino acids, are more conserved than others.
- ✓ Such conserved regions are often conserved because they encode a part of the protein that is functionally important.
- ✓ The term *motif* is used to refer to a part of a protein sequence that is associated with a particular biological function.
- ✓ For example a region of a protein that binds ATP is called an ATP binding *motif*. ❖
- ✓ Since these regions are conserved, they may be recognisable by the presence of a particular sequence of amino acids called a *pattern*.
- ✓ A pattern is thus a qualitative description of a motif in terms of amino acid sequence.

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- ✓ The concept of a *profile* extends this concept, allowing a quantitative description of a motif, by assigning probabilities to the occurrence of a particular amino acid at each position of a motif.
- ✓ Thus profiles can be used to describe very divergent motifs.
- ✓ The presence of a particular motif within a protein sequence can be used to suggest functions for uncharacterised proteins.
- ✓ A number of databases have been constructed that attempt to describe particular protein motifs in terms of patterns and profiles.




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✓ Search for patterns or profiles that are indicative of particular functional motifs within a query protein.

✓ Some examples of such databases include:

✓  PROSITE - a collection of patterns and profiles

✓  Pfam - A collection of Profiles generated using hidden Markov models

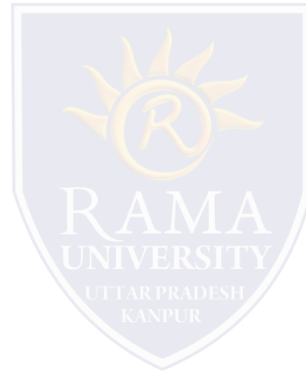
✓  PRINTS - provider of fingerprints (groups of aligned, un-weighted motifs)

✓  BLOCKS - a database of weighted profiles or blocks



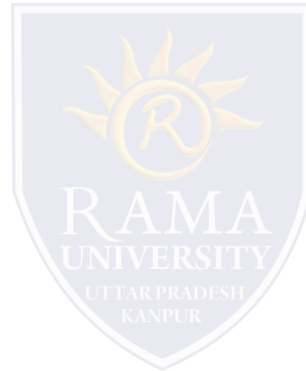
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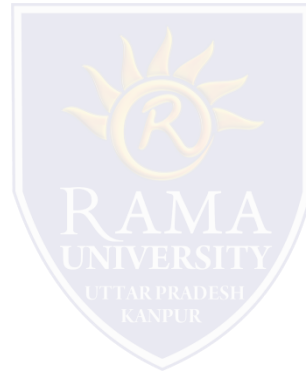
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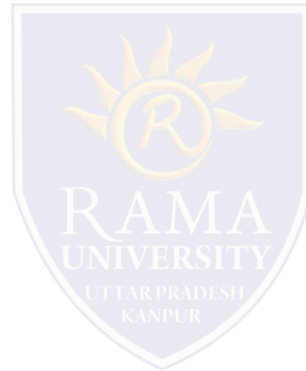
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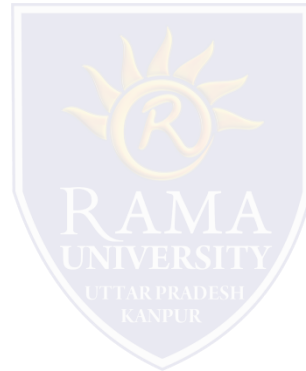
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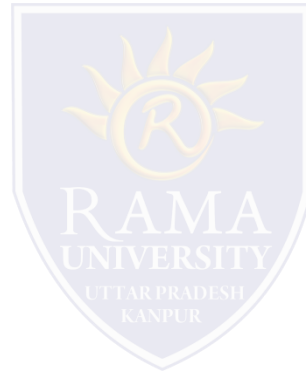
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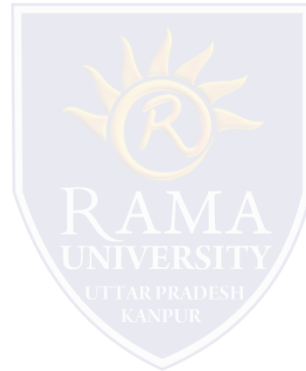
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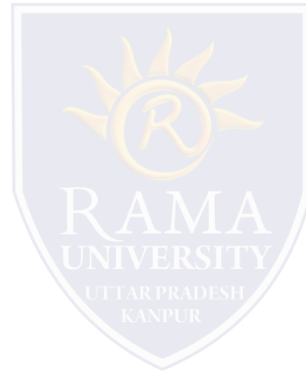
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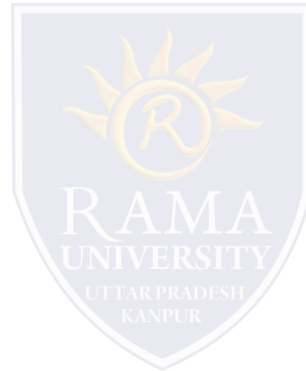
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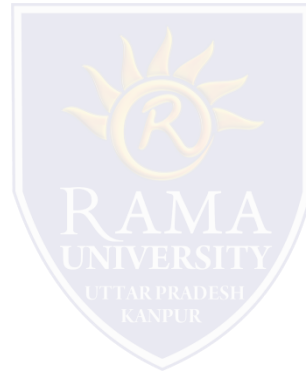
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# MCQs

1. A
2. A
3. A
4. A
5. A
6. A
7. A
8. A
9. A
10. A

